



SEQUENCE LISTING

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<120> MUTANTS OF STREPTOCOCCAL TOXIN C AND METHODS OF USE

<130> 600.347USI1

<140> US 09/336,036

<141> 1999-06-18

<150> US 09/308,829

<151> 1999-07-14

<150> US 60/091,864

<151> 1998-07-06

<150> PCT/US97/22125

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<150> US 60/033,251

<151> 1996-12-06

<160> 2

<170> PatentIn version 3.1

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<212> DNA

<213> Streptococcus pyogenes

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<221> CDS

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cgtacgagta atacatttaa ttaaggagaa aaa atg aaa aag att aac atc atc 174
Met Lys Lys Ile Asn Ile Ile
1 5
aaa ata gtt ttc ata att aca gtc ata ctg att tct act tat ttc acc 222
Lys Ile Val Phe Ile Ile Thr Val Ile Leu Ile Ser Thr Tyr Phe Thr
10 15 20
tat cat caa agt gac tct aag aaa gac att tcg aat gtt aaa agt gat 270
Tyr His Gln Ser Asp Ser Lys Lys Asp Ile Ser Asn Val Lys Ser Asp
25 30 35
tta ctt tat gca tac act ata act cct tat gat tat aaa gat tgc agg 318
Leu Leu Tyr Ala Tyr Thr Ile Thr Pro Tyr Asp Tyr Lys Asp Cys Arg

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gta aat ttt tca acg aca cac aca tta aac att gat act caa aaa tat				366
Val Asn Phe Ser	Thr Thr His Thr	Leu Asn Ile Asp	Thr Gln Lys Tyr	
	60	65	70	
aga ggg aaa gac tat tat att agt tcc gaa atg tct tat gag gcc tct				414
Arg Gly Lys Asp	Tyr Tyr Ile Ser	Ser Glu Met Ser	Tyr Glu Ala Ser	
	75	80	85	
caa aaa ttt aaa cga gat gat cat gta gat gtt ttt gga tta ttt tat				462
Gln Lys Phe Lys Arg Asp Asp	His Val Asp Val Phe	Gly Leu Phe Tyr		
	90	95	100	
att ctt aat tct cac acc ggt gag tac atc tat gga gga att acg cct				510
Ile Leu Asn Ser His Thr Gly Glu Tyr Ile Tyr		Gly Gly Ile Thr Pro		
	105	110	115	
gct caa aat aat aaa gta aat cat aaa tta ttg gga aat cta ttt att				558
Ala Gln Asn Asn Lys Val Asn His Lys Leu Leu Gly Asn Leu Phe Ile				
	120	125	130	135
tcg gga gaa tct caa cag aac tta aat aac aag att att cta gaa aag				606
Ser Gly Glu Ser Gln Gln Asn Leu Asn Asn Lys Ile Ile Leu Glu Lys				
	140	145	150	
gat atc gta act ttc cag gaa att gac ttt aaa atc aga aaa tac ctt				654
Asp Ile Val Thr Phe Gln Glu Ile Asp Phe Lys Ile Arg Lys Tyr Leu				
	155	160	165	
atg gat aat tat aaa att tat gac gct act tct cct tat gta agc ggc				702
Met Asp Asn Tyr Lys Ile Tyr Asp Ala Thr Ser Pro Tyr Val Ser Gly				
	170	175	180	
aga atc gaa att ggc aca aaa gat ggg aaa cat gag caa ata gac tta				750
Arg Ile Glu Ile Gly Thr Lys Asp Gly Lys His Glu Gln Ile Asp Leu				
	185	190	195	
ttt gac tca cca aat gaa ggg act aga tca gat att ttt gca aaa tat				798
Phe Asp Ser Pro Asn Glu Gly Thr Arg Ser Asp Ile Phe Ala Lys Tyr				
	200	205	210	215
aaa gat aat aga att atc aat atg aag aac ttt agt cat ttc gat att				846
Lys Asp Asn Arg Ile Ile Asn Met Lys Asn Phe Ser His Phe Asp Ile				
	220	225	230	
tat ctt gaa aaa taattcatca tacacaaaaa accgccccaga ataattctgag				898
Tyr Leu Glu Lys				
	235			
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Ile Ser Asn Val Lys Ser Asp Leu Leu Tyr Ala Tyr Thr Ile Thr Pro
 35 40 45

Tyr Asp Tyr Lys Asp Cys Arg Val Asn Phe Ser Thr Thr His Thr Leu
 50 55 60

Asn Ile Asp Thr Gln Lys Tyr Arg Gly Lys Asp Tyr Tyr Ile Ser Ser
 65 70 75 80

Glu Met Ser Tyr Glu Ala Ser Gln Lys Phe Lys Arg Asp Asp His Val
 85 90 95

Asp Val Phe Gly Leu Phe Tyr Ile Leu Asn Ser His Thr Gly Glu Tyr
 100 105 110

Ile Tyr Gly Gly Ile Thr Pro Ala Gln Asn Asn Lys Val Asn His Lys
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 130 135 140

Asn Lys Ile Ile Leu Glu Lys Asp Ile Val Thr Phe Gln Glu Ile Asp
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Phe Lys Ile Arg Lys Tyr Leu Met Asp Asn Tyr Lys Ile Tyr Asp Ala
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Thr Ser Pro Tyr Val Ser Gly Arg Ile Glu Ile Gly Thr Lys Asp Gly
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Lys His Glu Gln Ile Asp Leu Phe Asp Ser Pro Asn Glu Gly Thr Arg
 195 200 205

Ser Asp Ile Phe Ala Lys Tyr Lys Asp Asn Arg Ile Ile Asn Met Lys
 210 215 220

Asn Phe Ser His Phe Asp Ile Tyr Leu Glu Lys
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